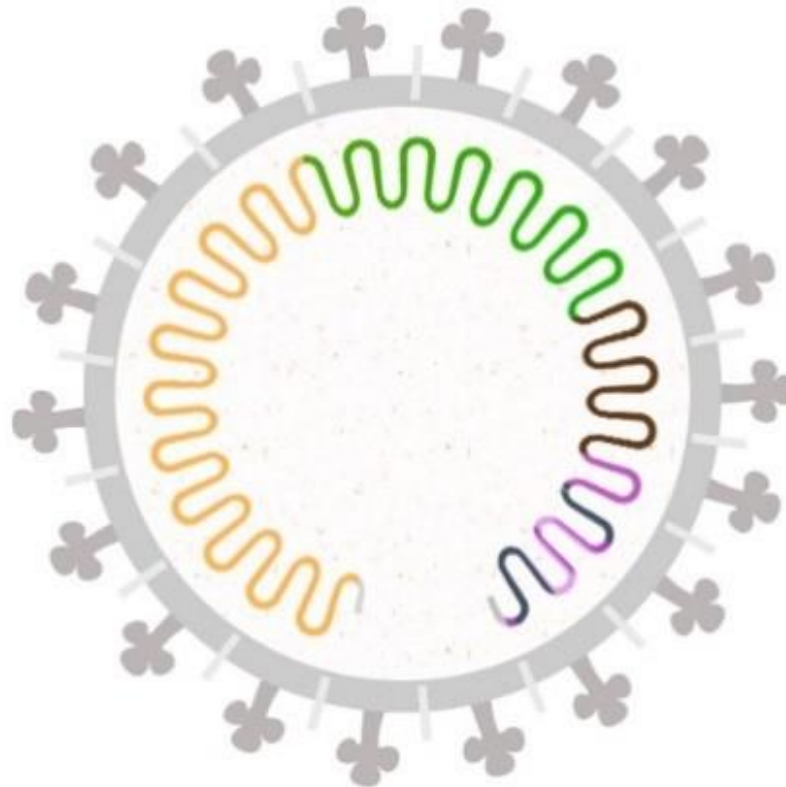


Variants of SARS-CoV-2



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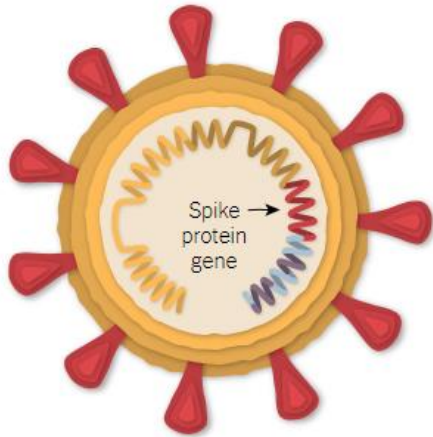
Slide layout & past information provided by Kara Levinson, PhD, MPH, D(ABMM)

Deputy Director, TN Public Health Laboratory

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What we know:

- Viruses mutate during genome replication
 - Mutations = changes in genome over time
 - SARS-CoV-2 acquires ~1-2 new mutations every month
 - Variant = has mutations that differentiate it from predominant strain circulating in the population
 - Lineage = group of variants with similar genetic changes and common ancestor



CORONAVIRUS
GENOME

ORF1a
protein

ORF1b
protein

Spike
protein

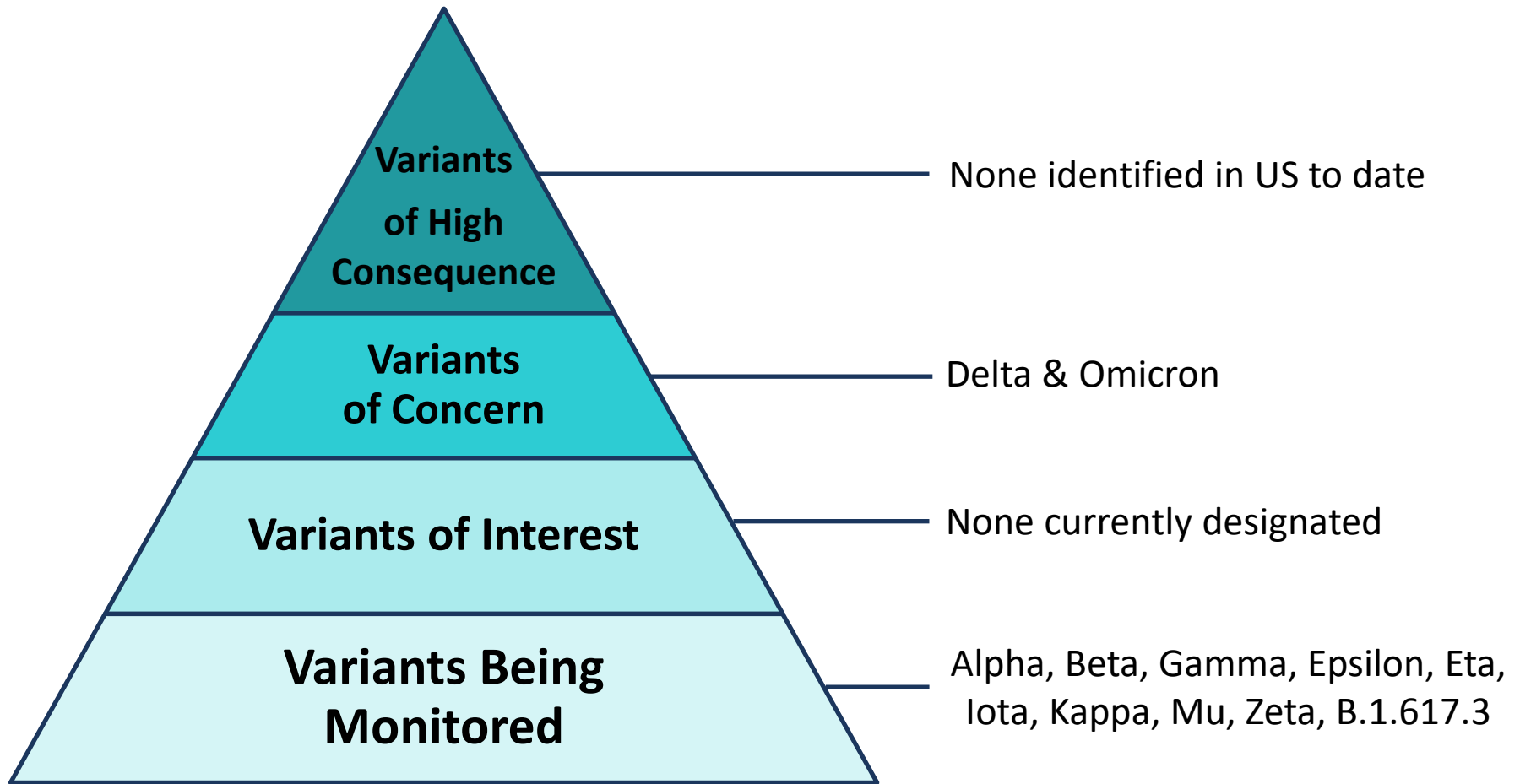
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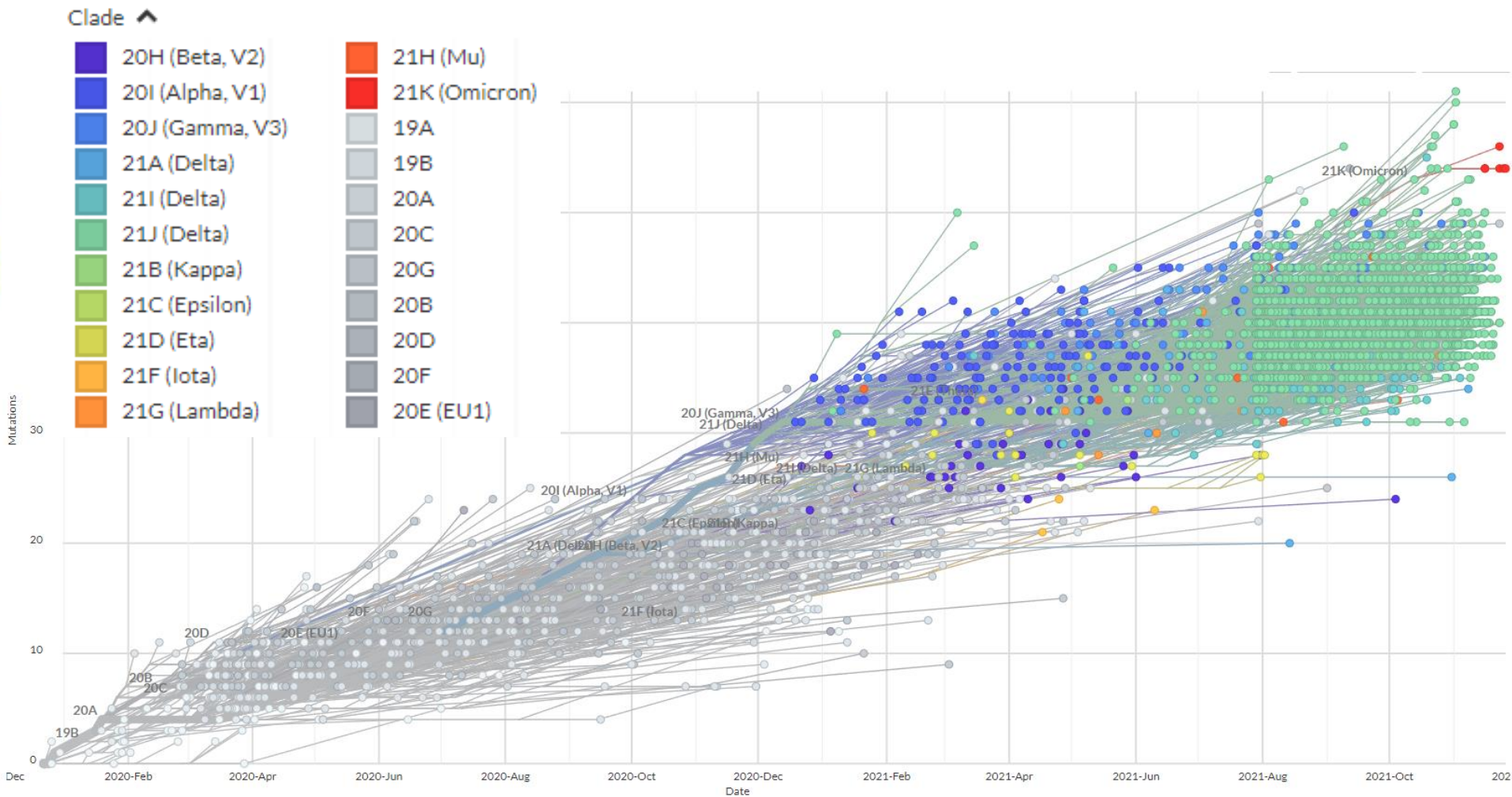
<https://www.nytimes.com/2020/12/21/health/new-covid-strain-uk.html>

What we know:

- SIG Variant classification scheme



Genomic epidemiology of SARS-CoV-2

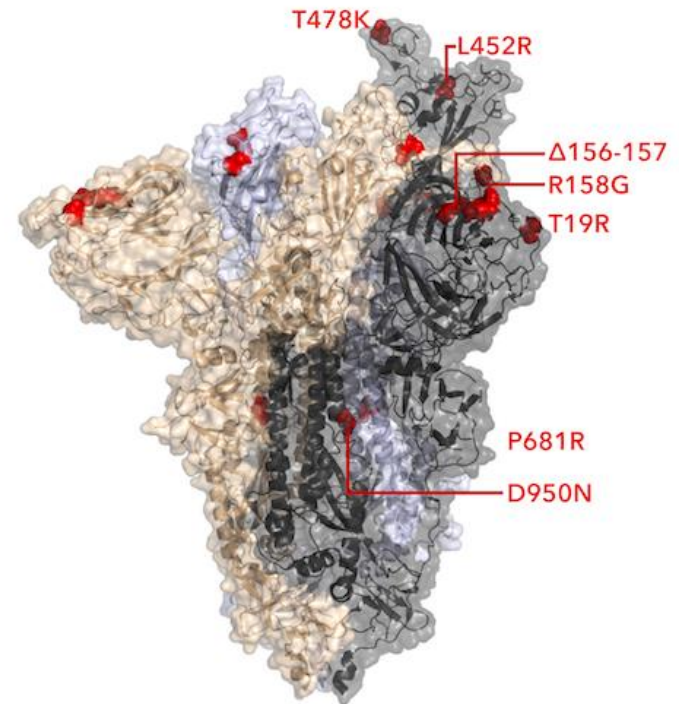


<https://nextstrain.org/ncov/global>

B.1.167.2 & AY Lineages (Delta)

- 13 mutations
 - 9 in spike protein
- Increase in severity of illness
 - More likely to be hospitalized
- 2X more contagious
- AY.1 and AY.2 lineages are not susceptible to some monoclonal antibody treatments, but most other delta lineages are to those with EUA
- Reduction in neutralization by post-vaccination sera

Spike protein mutations (Delta: B.1.617.2)

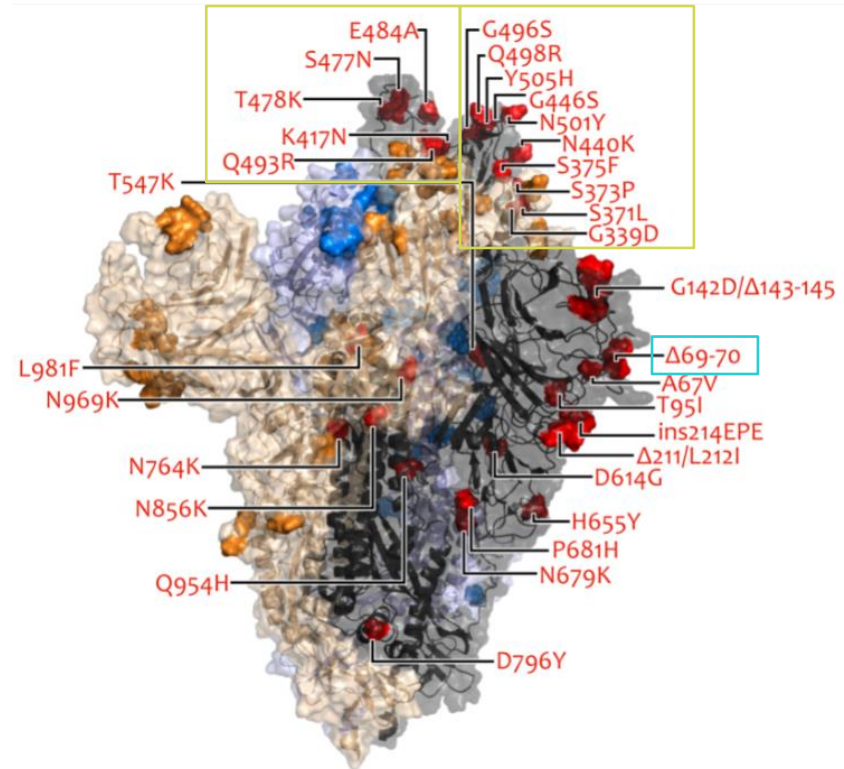


[COG-UK/Mutation Explorer \(gla.ac.uk\)](https://cog-uk.github.io/MutationExplorer/)

B.1.1.529 (Omicron)

- About 50 mutations not seen in combination before
 - 30+ mutations in spike protein, 15 of which are in RBD
- Unknown impact on severity of illness, vaccine-induced immunity, or immunity from previous infection
- *May* have increased transmissibility
 - Predominate variant in South Africa, replacing Delta
- Deletion of H69, V70 reduces S-gene target sensitivity of TaqPath COVID-19 Combo kit
 - SGTF for specimen may be omicron, but must be confirmed by sequencing

Spike protein mutations (Omicron: B.1.1.529)



[COG-UK/Mutation Explorer \(gla.ac.uk\)](https://cog-uk.github.io/MutationExplorer/)

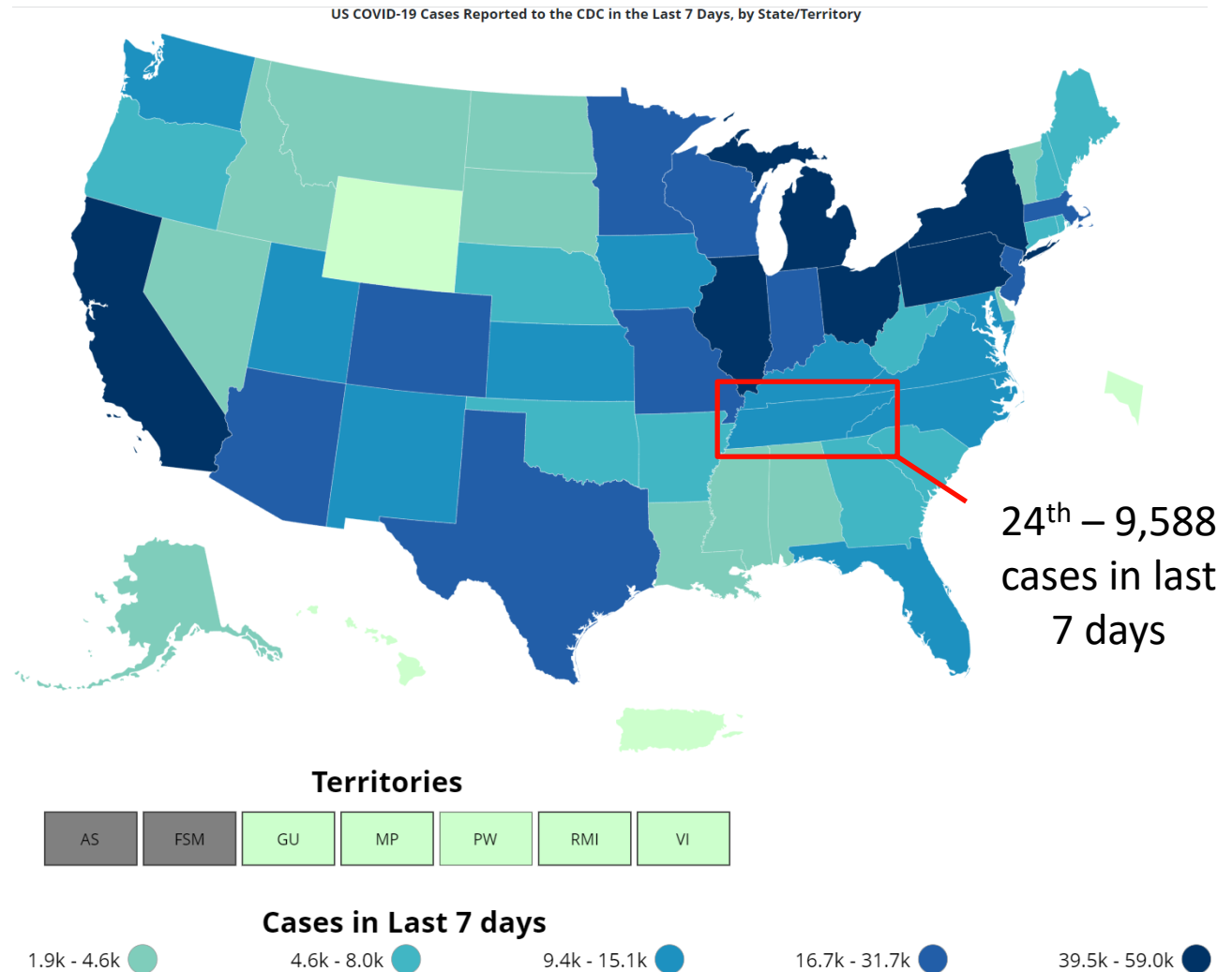
Summary of current variants

<u>Name</u>	<u>Earliest Sample Date</u>	<u>Cases in US</u>	<u># of countries reporting cases</u>	<u>Key Mutations</u>	<u>Transmissibility Rate</u>
B.1.1.7 Alpha	09/20	Yes	175	ΔH69-V70, N501Y, D614G, P681H	50% greater
B.1.351 Beta	09/20	Yes	114	K417N, E484K, N501Y, D614G,	50% greater
P.1 Gamma	10/20	Yes	74	K417T, E484K, N501Y, D614G	Higher viral load & greater transmissibility
B.1.617.2 Delta	03/21	Yes	148	T19R, ΔE156-F157, L452R, T478K, D614G, P681R	2X greater than original
B.1.1.529 Omicron	11/21	Yes	34	ΔH69-V70, K417N, N440K, G446S, S477N, T478K, E484A, Q493K, G496S, Q498R, N501Y, Y505H, D614G, P681H	Currently unknown

PANGO Lineages (https://cov-lineages.org/index.html#global_reports), CDC MMWR (<https://www.cdc.gov/mmwr/volumes/70/wr/mm7003e2.htm>), Global Virus Network (<https://gvn.org/covid-19/omicron-b-1-1-529/#>)

US COVID-19 cases

- More than 91% of current cases are caused by B.1.617.2 Delta Variant
- Omicron ~3% of current cases
- Other Delta AY Lineages account for remaining cases



https://covid.cdc.gov/covid-data-tracker/#cases_last7-count

What are we doing about it?

Sequencing!

- National SARS-CoV-2 Strain Surveillance (NS3) system
 - CDC contracts with large commercial labs (LabCorp, Quest, Path Group)
 - CDC funds 29 universities to conduct genomic surveillance research
 - SPHERES, a national consortium of laboratories sequencing SARS-CoV-2
 - n = 250 institutions, including academic centers, industry, non-governmental organizations, & public health agencies
 - led by CDC's Advanced Molecular Detection (AMD) program
 - TN PHL submits SARS-CoV-2 positive specimens weekly (avg. 5-15) after WGS is completed on site
 - most patient samples are now tested by reference labs & universities throughout the state

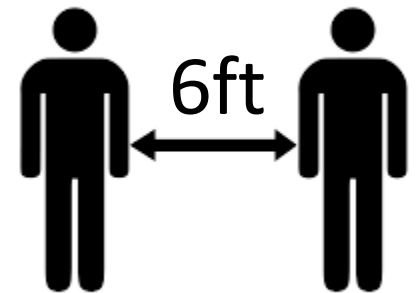
CDC NS3 Enhanced Surveillance efforts

- B.1.1.529 (Omicron)
 - Some samples present SGTF, but not all (Samples sent to CDC should not solely focus on SGTF)
- Additional new variants
 - CDC requires approval for sample submission
- Vaccine breakthroughs
 - Defined as positive SARS-CoV-2 RNA or Ag test detected from a respiratory specimen collected ≥ 14 d after completing full vaccine series
 - Can send up to 20 samples weekly to CDC
- All other previous variants are no longer requested by CDC

<https://www.aphl.org/programs/preparedness/Crisis-Management/Documents/NS3-Submission-Guidance.pdf>

How to stop SARS-CoV-2 variant emergence

Trans~~mission~~ → Infection → Viral Replication → Mutation



Questions?

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